

CLAIMS

1. A method of constructing a variant of a parent *Coprinus* laccase, which variant has laccase activity and increased oxidation potential and/or altered pH optimum and/or altered mediator pathway and/or altered O_2/OH^- -pathway as compared to said parent laccase, which method comprises

i) analysing the three-dimensional structure of the parent *Coprinus* laccase to identify at least one amino acid residue or at least one structural part of the *Coprinus* laccase structure, which amino acid residue or structural part is believed to be of relevance for altering the oxidation potential and/or altering the pH optimum and/or altering the mediator pathway and/or altering the O_2/OH^- -pathway of the parent *Coprinus* laccase (as evaluated on the basis of structural or functional considerations),

ii) constructing a *Coprinus* laccase variant, which as compared to the parent *Coprinus* laccase, has been modified in the amino acid residue or structural part identified in i) so as to alter the oxidation potential and/or alter the pH optimum and/or alter the mediator pathway and/or alter the O_2/OH^- -pathway, and, optionally,

iii) testing the resulting *Coprinus* laccase variant with respect to oxidation potential and/or pH optimum and/or mediator pathway and/or O_2/OH^- -pathway.

2. A variant of a parent *Coprinus* laccase, which variant has increased oxidation potential and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:

G411A, V, P, L, I, F, Y, W;

G412A, V, P, L, I, F, Y, W;

V409P, L, I, F, Y, W;

T257A, V, P, L, I, F, Y, W;

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F358Y, W, I;

T359A, V, P, L, I, F, Y, W;

L480I, F, Y, W;

L351 I, F, Y, W;

5 E473A, V, P, L, I, F, Y, W;

D98A, V, P, L, I, F, Y, W;

G131A, V, P, L, I, F, Y, W;

D443A, V, P, L, I, F, Y, W;

R260 A, V, P, L, I, F, Y, W.

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3. A variant of a parent *Coprinus* laccase, which variant has an altered pH optimum and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:

15 180-181;

222-224;

257;

281-284;

352-353;

20 357-358;

409-416;

470-490.

4. A variant of a parent *Coprinus* laccase, which variant has an altered mediator efficiency and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:

179-182;

223;

30 281-282;

353-358;

410-412;

472;

474-475;

35 477-478.

5. A method of constructing a variant of a parent *Coprinus*-like laccase, which variant has laccase activity and increased

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oxidation potential and/or changed pH optimum and/or altered mediator pathway and/or altered O_2/OH^- -pathway as compared to said parent laccase, which method comprises

i) comparing the three-dimensional amino acid structure of the *Coprinus* laccase with an amino acid sequence of a *Coprinus*-like laccase,

ii) identifying a part of the *Coprinus*-like laccase amino acid sequence which is different from the *Coprinus* laccase amino acid sequence and which from structural or functional considerations is contemplated to be responsible for differences in the stability of the *Coprinus* and *Coprinus*-like laccase,

iii) modifying the part of the *Coprinus*-like laccase identified in ii) whereby a *Coprinus*-like laccase variant is obtained, which has an increased oxidation potential and/or changed pH optimum and/or altered mediator pathway and/or altered O_2/OH^- -pathway as compared to the parent *Coprinus*-like laccase, and optionally,

iv) testing the resulting *Coprinus*-like laccase variant with respect to oxidation potential and/or pH optimum and/or mediator pathway and/or O_2/OH^- -pathway.

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6. The method according to claim 5, wherein, in step iii), the part of the *Coprinus*-like laccase is modified so as to resemble the corresponding part of the *Coprinus* laccase.

7. The method according to claim 5 or 6, wherein, in step iii), the modification is accomplished by deleting one or more amino acid residues of the part of the *Coprinus*-like laccase to be modified; or the modification is accomplished by replacing one or more amino acid residues of the part of the *Coprinus*-like laccase to be modified with the amino acid residues occupying corresponding positions in the *Coprinus* laccase; or the

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[illegible]

9. The method according to claim 1 or 5, wherein the parent *Coprinus laccase* is derived from a strain of *Coprinus cinereus*.

11. A variant of a parent *Polyporus pinsitus* (I) laccase, which variant has an increased oxidation potential and comprises a mutation in a position corresponding to at least one of the 20 following positions in SEQ ID No. 2:

25 12. A variant of a parent *Polyporus pinsitus* (I) laccase, which variant has an altered pH optimum and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:

30 ~~F~~463L, M.

G392A;

A461T,S;
N260Q,Y;
G165K,R.

5 14. A variant of a parent *Polyporus pinsitus* (I) laccase, which variant has an altered O₂/OH⁻ pathway and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:

F81D,E;
10 L112D,E;
A80D,E.

15. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an increased oxidation potential and 15 comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:

G511A,V,P,L,I,F,Y,W;
T428A,V,P,L,I,F,Y,W;
S510A,V,P,L,I,F,Y,W;
20 D106A,V,P,L,I,F,Y,W;
N109A,V,P,L,I,F,Y,W,Q;
L500I,F,Y,W;
A108V,P,L,I,F,Y,W;
G514A,V,P,L,I,F,Y,W.

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16. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an altered pH optimum and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:

30 192-193;
234-236;
269;
293-294;
364-365;
35 372-373;
426-433;
503-513.

17. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an altered mediator efficiency and comprises a mutation in a position corresponding to at least one of the 5 following positions in SEQ ID No. 10:

185-194;
235;
293-294;
365-373;
10 427-429;
505;
507-508;
510-511.

15 18. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an altered O₂/OH-pathway and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:

A506E;
20 N109D;
H93E;
H95E;
M433E;
M480E.

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19. A DNA construct comprising a DNA sequence encoding a laccase variant according to claim 2 or claims 11-18.

20. A recombinant expression vector which carries a DNA construct according to claim 19.

21. A cell which is transformed with a DNA construct according to claim 19 or a vector according to claim 20.

35 22. A cell according to claim 21, which is a microorganism.

23. A cell according to claim 22, which is a bacterium or a fungus.

24. A cell according to claim 23, which is an *Aspergillus niger* or an *Aspergillus oryzae* cell.
- 5 25. Use of a laccase variant according to claim 2 or claims 11-18 for oxidizing a substrate.
26. Use of a laccase variant according to claim 2 or claims 11-18 for dye transfer inhibition.
- 10 27. Use of a laccase variant according to claim 2 or claims 11-18 for bleaching textiles, in particular for bleaching denim.
28. A detergent additive comprising a laccase variant according 15 to claim 2 or claims 11-18 in the form of a non-dusting granulate, a stabilised liquid or a protected enzyme.
29. A detergent additive according to claim 28, which additionally comprises one or more other enzyme such as a 20 protease, a lipase, an amylase, and/or a cellulase.
30. A detergent composition comprising a laccase variant according to claim 2 or claims 11-18 and a surfactant.
- 25 31. A detergent composition according to claim 30 which additionally comprises one or more other enzymes such as a protease, a lipase, an amylase and/or a cellulase.

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